The University of Chicago
Committee on Virology

Bernard Roizman, ScD.
Joseph Regenstein Professor
of Virology

May 2, 1985

Dr. Harold E. Varmus
American Cancer Society
University of California
School of Medicine
Department of Microbiology
and Immunology
San Francisco, CA 94143

Dear Harold,

I am responding to your letter regarding retrovirus classification. The response is broader than your questions:

First, my experience with classification of herpesviruses:

1. Once a name becomes established (eg. Epstein-Barr, herpes simplex, cytomegalovirus), it is difficult to get rid of it. In these instances the viruses were named after Epstein and Barr, a disease, and cytopathology. You cannot get rid of them, but you should nevertheless introduce formal names that avoid the problems listed above.

2. For the last 20 years many herpesviruses were designated according to species from which they were isolated. This is not a bad idea particularly because many viruses have a preferred host even if they do cross species. It is easier to keep track of them by host name.

3. We came up with the following scheme:

A: family HERPESVIRIDAE

Subfamily:	Alphaherpesvirinae Betaherpesvirinae Gammaherpsvirinae	Classification basis: biologic properties
Genus:	several in each subfamily	Classification basis: (a) genome structure (b) sequence homology (c) serologic relatedness (at least 2 of 3 characteristics to be included in the same genus
Species:	one to several in each genus	Nomeclature and classification: (a) primary host (b) serially, by isolation without regard to subfamily or genus (c) signifcant evolutionary divergence (minimum requirement: totally different DNA restriction patterns)

Eg: Human herpesvirus 1 (alphaherpesvirinae) simplex 1
Human herpesvirus 2 " 2
Human herpesvirus 3 " Varicella-zoster
Human herpesvirus 4 (Gammaherpesvirinae) Epstein-Barr
Human herpesvirus 5 (Betaherpesvirinae) Cytomegalovirus

My advice with respect to retroviruses is as follows:

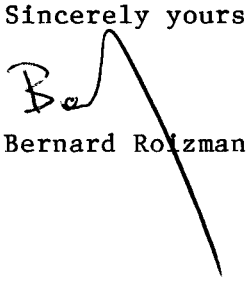
1. It makes sense to subdivide the family into subfamily on the basis of biologic characteristics. If you use more stringent criteria, you will have no flexibility. For example, the presence of an extra gene may be a desirable characteristic for classification, but if the biology does not correspond to the group in which it is placed, no one will will take the classification seriously.
2. Subordinate the biologic properties to molecular properties within each subfamily.
3. Avoid the name of diseases or host cell (HTLV has to go!), but do use human, etc and label them sequentially. The reason for the latter is that someone will give a new virus an inappropriate name and by the time the virus is properly characterized two years down the road the name sticks..... A serial number for a given host is neutral with respect to properties. Thus HR1, HR2, HR3 for human retroviruses 1, 2 and 3 is appropriate and does not prejudice the likelihood that HR1 and HR2 will end up in one genus of one subfamily whereas HR3 may end up in a different subfamily and genus.

3. Hepatatis A, poliovirus, etc are inappropriate, but are historically defensible - the names have been around too long. They would not have been approved today. Aids virus is definitely not appropriate since it is likely that non-aids retroviruses with similar properties may emerge in the future. The classification has nothing to do with the patient-physician relationship: no matter what you call it the physician may have to disclose to the patient the potential transmissibility of the infection etc.

I do not know if I have answered everything!

With best regards,

Sincerely yours



Bernard Roizman

BR:ms